

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

- 5 (A) NAME: SOLVAY (Société Anonyme)  
(B) STREET: rue du Prince Albert, 33  
(C) CITY: Brussels  
(E) COUNTRY: Belgium  
(F) POSTAL CODE: 1050  
(G) TELEPHONE: (02) 509.61.11

- 10 (ii) TITLE OF INVENTION: Xylanase, microorganisms  
producing it, DNA molecule [sic], methods for preparing  
this xylanase and uses of the latter

(iii) NUMBER OF SEQUENCES: 29

(iv) COMPUTER READABLE FORM:

- 15 (A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS: MS-DOS

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 663 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

- 25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CAAATCGTCA CCGACAATTC CATTGGCAAC CACGATGGCT ATGATTATGA ATTTGGAAA

GATAGCGGTG GCTCTGGGAC AATGATTCTC AATCATGGCG GTACGTTTCAG TGCCCAATGG	120
AACAATGTTA ACAACATATT ATTCCGTAAA GGTA AAAAAT TCAATGAAAC ACAACACAC	180
CAACAAGTTG GTAACATGTC CATAAACTAC GGAGCCAAC TCCAACCAAA TGGTAATGCG	240
TATTTATGCG TCTATGGTTG GACTGTTGAC CCTCTTGTCG AATATTATAT TGTCGACAGT	300
TGGGGCAACT GCGTCCACC AGGAGCAACG CTAAGGGGA CCATCACTGT TGATGGAGGA	360
ACATATGATA TCTACGAGAC TCTTAGAGTC AATCAACCCT CCATTAAGGG GATTGCCACA	420
TTTAAACAAT ATTGGAGTGT TCGAAGATCG AAACGCACGA GTGGCACGAT TTCTGTCAGC	480
AACCACTTTA GAGCGTGGGA AAACCTTAGGG ATGAATATGG GGAAAATGTA TGAAGTCGCG	540
CTTACTGTAG AAGGCTATCA AAGTAGCGGA AGTGCTAATG TATATAGCAA TACTAAGA	600
ATTAACGGTA ACCCTCTCTC AACTATTAGT AATGACGAGA GCATAACTTT GGATAAAAAC	660
AAT	663

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 663 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CAA ATC GTC ACC GAC AAT TCC ATT GGC AAC CAC GAT GGC TAT GAT TAT 48  
Gln Ile Val Thr Asp Asn Ser Ile Gly Asn His Asp Gly Tyr Asp Tyr  
1 5 10 15

GAA TTT TGG AAA GAT AGC GGT GGC TCT GGG ACA ATG ATT CTC AAT CAT 96  
Glu Phe Trp Lys Asp Ser Gly Gly Ser Gly Thr Met Ile Leu Asn His  
20 25 30

GGC GGT ACG TTC AGT GCC CAA TGG AAC AAT GTT AAC AAC ATA TTA TTC 144  
Gly Gly Thr Phe Ser Ala Gln Trp Asn Asn Val Asn Asn Ile Leu Phe  
35 40 45

CGT AAA GGT AAA AAA TTC AAT GAA ACA CAA ACA CAC CAA CAA GTT GGT 192  
Arg Lys Gly Lys Lys Phe Asn Glu Thr Gln Thr His Gln Gln Val Gly  
50 55 60

AAC ATG TCC ATA AAC TAC GGA GCC AAC TTC CAA CCA AAT GGT AAT GCG 240  
Asn Met Ser Ile Asn Tyr Gly Ala Asn Phe Gln Pro Asn Gly Asn Ala  
65 70 75 80

TAT TTA TGC GTC TAT GGT TGG ACT GTT GAC CCT CTT GTC GAA TAT TAT 288  
Tyr Leu Cys Val Tyr Gly Trp Thr Val Asp Pro Leu Val Glu Tyr Tyr  
85 90 95

ATT GTC GAC AGT TGG GGC AAC TGG CGT CCA CCA GGA GCA ACG CCT AAG 336  
Ile Val Asp Ser Trp Gly Asn Trp Arg Pro Pro Gly Ala Thr Pro Lys  
100 105 110

GGG ACC ATC ACT GTT GAT GGA GGA ACA TAT GAT ATC TAC GAG ACT CTT 384  
Gly Thr Ile Thr Val Asp Gly Gly Thr Tyr Asp Ile Tyr Glu Thr Leu  
115 120 125

AGA GTC AAT CAA CCC TCC ATT AAG GGG ATT GCC ACA TTT AAA CAA TAT 432  
Arg Val Asn Gln Pro Ser Ile Lys Gly Ile Ala Thr Phe Lys Gln Tyr  
130 135 140

TGG AGT GTT CGA AGA TCG AAA CGC ACG AGT GGC ACG ATT TCT GTC AGC 480  
Trp Ser Val Arg Arg Ser Lys Arg Thr Ser Gly Thr Ile Ser Val Ser  
145 150 155 160

AAC CAC TTT AGA GCG TGG GAA AAC TTA GGG ATG AAT ATG GGG AAA ATG 528  
Asn His Phe Arg Ala Trp Glu Asn Leu Gly Met Asn Met Gly Lys Met  
165 170 175

TAT GAA GTC GCG CTT ACT GTA GAA GGC TAT CAA AGT AGC GGA AGT GCT 576  
Tyr Glu Val Ala Leu Thr Val Glu Gly Tyr Gln Ser Ser Gly Ser Ala  
180 185 190

AAT GTA TAT AGC AAT ACA CTA AGA ATT AAC GGT AAC CCT CTC TCA ACT 624  
Asn Val Tyr Ser Asn Thr Leu Arg Ile Asn Gly Asn Pro Leu Ser Thr  
195 200 205

ATT AGT AAT GAC GAG AGC ATA ACT TTG GAT AAA AAC AAT 663  
Ile Ser Asn Asp Glu Ser Ile Thr Leu Asp Lys Asn Asn  
210 215 220

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 221 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal fragment

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Bacillus
- (B) STRAIN: 720/1

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Gln Ile Val Thr Asp Asn Ser Ile Gly Asn His Asp Gly Tyr Asp Tyr  
1 5 10 15

Glu Phe Trp Lys Asp Ser Gly Gly Ser Gly Thr Met Ile Leu Asn His  
20 25 30

Gly Gly Thr Phe Ser Ala Gln Trp Asn Asn Val Asn Asn Ile Leu Phe  
35 40 45

Arg Lys Gly Lys Lys Phe Asn Glu Thr Gln Thr His Gln Gln Val Gly  
50 55 60

Asn Met Ser Ile Asn Tyr Gly Ala Asn Phe Gln Pro Asn Gly Asn Ala  
65 70 75 80

Tyr Leu Cys Val Tyr Gly Trp Thr Val Asp Pro Leu Val Glu Tyr Tyr  
85 90 95

Ile Val Asp Ser Trp Gly Asn Trp Arg Pro Pro Gly Ala Thr Pro Lys  
100 105 110

Gly Thr Ile Thr Val Asp Gly Gly Thr Tyr Asp Ile Tyr Glu Thr Leu  
115 120 125

Arg Val Asn Gln Pro Ser Ile Lys Gly Ile Ala Thr Phe Lys Gln Tyr  
130 135 140

Trp Ser Val Arg Arg Ser Lys Arg Thr Ser Gly Thr Ile Ser Val Ser  
145 150 155 160

Asn His Phe Arg Ala Trp Glu Asn Leu Gly Met Asn Met Gly Lys Met  
165 170 175

Tyr Glu Val Ala Leu Thr Val Glu Gly Tyr Gln Ser Ser Gly Ser Ala  
180 185 190

Asn Val Tyr Ser Asn Thr Leu Arg Ile Asn Gly Asn Pro Leu Ser Thr  
195 200 205

Ile Ser Asn Asp Glu Ser Ile Thr Leu Asp Lys Asn Asn  
210 215 220

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 744 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

ATGAGACAAA AGAAATTGAC GTTGATTTTA GCCTTTTITAG TTTGTTTTGC ACTAACCTTA 60  
CCTGCAGAAA TAATTCAGGC ACAAATCGTC ACCGACAATT CCATTGGCAA CCACGATGGC 120  
TATGATTATG AATTTTGGAA AGATAGCGGT GGCTCTGGGA CAATGATTCT CAATCATGGC 180  
GGTACGTTCA GTGCCCAATG GAACAATGTT AACAACATAT TATTCCGTAA AGGTAAAAAA 240  
TTCAATGAAA CACAAACACA CCAACAAGTT GGTAACATGT CCATAAACTA CGGAGCCAAC 300  
TTCCAACCAA ATGGTAATGC GTATTTATGC GTCTATGGTT GGA CTGTTGA CCCTCTTGTC 360  
GAATATTATA TTGTCGACAG TTGGGGCAAC TGGCGTCCAC CAGGAGCAAC GCCTAAGGGG 420  
ACCATCACTG TTGATGGAGG AACATATGAT ATCTACGAGA CTCTTAGAGT CAATCAACCC 480  
TCCATTAAGG GGATTGCCAC ATTTAAACAA TATTGGAGTG TTCGAAGATC GAAACGCACG 540  
AGTGGCACGA TTTCTGTCAG CAACCACTTT AGAGCGTGGG AAAACTTAGG GATGAATATG 600

GGGAAAATGT ATGAAGTCGC GCTTACTGTA GAAGGCTATC AAAGTAGCGG AAGTGCTAAT 660

GSTATATAGCA ATACACTAAG AATTAAACGGT AACCTCTCTCT CAACTATTAG TAATGACGAG 720

AGCATAACTT TGGATAAAAA CAAT 744

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 744 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATG AGA CAA AAG AAA TTG ACG TTG ATT TTA GCC TTT TTA GTT TGT TTT 48  
Met Arg Gln Lys Lys Leu Thr Leu Ile Leu Ala Phe Leu Val Cys Phe  
-25 -20 -15

GCA CTA ACC TTA CCT GCA GAA ATA ATT CAG GCA CAA ATC GTC ACC GAC 96  
Ala Leu Thr Leu Pro Ala Glu Ile Ile Gln Ala Gln Ile Val Thr Asp  
-10 -5 -1 1 5

AAT TCC ATT GGC AAC CAC GAT GGC TAT GAT TAT GAA TTT TGG AAA GAT 144  
Asn Ser Ile Gly Asn His Asp Gly Tyr Asp Tyr Glu Phe Trp Lys Asp  
10 15 20

AGC GGT GGC TCT GGG ACA ATG ATT CTC AAT CAT GGC GGT ACG TTC AGT 92  
Ser Gly Gly Ser Gly Thr Met Ile Leu Asn His Gly Gly Thr Phe Ser  
25 30 35

GCC CAA TGG AAC AAT GTT AAC AAC ATA TTA TTC CGT AAA GGT AAA AAA	240
Ala Gln Trp Asn Asn Val Asn Asn Ile Leu Phe Arg Lys Gly Lys Lys	
40 45 50	
TTC AAT GAA ACA CAA ACA CAC CAA CAA GTT GGT AAC ATG TCC ATA AAC	288
Phe Asn Glu Thr Gln Thr His Gln Gln Val Gly Asn Met Ser Ile Asn	
55 60 65	
TAC GGA GCC AAC TTC CAA CCA AAT GGT AAT GCG TAT TTA TGC GTC TAT	336
Tyr Gly Ala Asn Phe Gln Pro Asn Gly Asn Ala Tyr Leu Cys Val Tyr	
70 75 80 85	
GGT TGG ACT GTT GAC CCT CTT GTC GAA TAT TAT ATT GTC GAC AGT TGG	384
Gly Trp Thr Val Asp Pro Leu Val Glu Tyr Tyr Ile Val Asp Ser Trp	
90 95 100	
GGC AAC TGG CGT CCA CCA GGA GCA ACG CCT AAG GGG ACC ATC ACT GTT	432
Gly Asn Trp Arg Pro Pro Gly Ala Thr Pro Lys Gly Thr Ile Thr Val	
105 110 115	
GAT GGA GGA ACA TAT GAT ATC TAC GAG ACT CTT AGA GTC AAT CAA CCC	480
Asp Gly Gly Thr Tyr Asp Ile Tyr Glu Thr Leu Arg Val Asn Gln Pro	
120 125 130	
TCC ATT AAG GGG ATT GCC ACA TTT AAA CAA TAT TGG AGT GTT CGA AGA	528
Ser Ile Lys Gly Ile Ala Thr Phe Lys Gln Tyr Trp Ser Val Arg Arg	
135 140 145	
TCG AAA CGC ACG AGT GGC ACG ATT TCT GTC AGC AAC CAC TTT AGA GCG	576
Ser Lys Arg Thr Ser Gly Thr Ile Ser Val Ser Asn His Phe Arg Ala	
150 155 160 165	
TGG GAA AAC TTA GGG ATG AAT ATG GGG AAA ATG TAT GAA GTC GCG CTT	624
Trp Glu Asn Leu Gly Met Asn Met Gly Lys Met Tyr Glu Val Ala Leu	
170 175 180	



ACT GTA GAA GGC TAT CAA AGT AGC GGA AGT GCT AAT GTA TAT AGC AAT 672  
 Thr Val Glu Gly Tyr Gln Ser Ser Gly Ser Ala Asn Val Tyr Ser Asn  
 185 190 195

ACA CTA AGA ATT AAC GGT AAC CCT CTC TCA ACT ATT AGT AAT GAC GAG 720  
 Thr Leu Arg Ile Asn Gly Asn Pro Leu Ser Thr Ile Ser Asn Asp Glu  
 200 205 210

AGC ATA ACT TTG GAT AAA AAC AAT 744  
 Ser Ile Thr Leu Asp Lys Asn Asn  
 215 220

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal fragment

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Bacillus  
 (B) SOURCE: 720/1

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Met Arg Gln Lys Lys Leu Thr Leu Ile Leu Ala Phe Leu Val Cys Phe  
 -25 -20 -15

Ala Leu Thr Leu Pro Ala Glu Ile Ile Gln Ala Gln Ile Val Thr Asp  
 -10 -5 -1 1 5

Asn Ser Ile Gly Asn His Asp Gly Tyr Asp Tyr Glu Phe Trp Lys Asp  
10 15 20

Ser Gly Gly Ser Gly Thr Met Ile Leu Asn His Gly Gly Thr Phe Ser  
25 30 35

Ala Gln Trp Asn Asn Val Asn Asn Ile Leu Phe Arg Lys Gly Lys Lys  
40 45 50

Phe Asn Glu Thr Gln Thr His Gln Gln Val Gly Asn Met Ser Ile Asn  
55 60 65

Tyr Gly Ala Asn Phe Gln Pro Asn Gly Asn Ala Tyr Leu Cys Val Tyr  
70 75 80 85

Gly Trp Thr Val Asp Pro Leu Val Glu Tyr Tyr Ile Val Asp Ser Trp  
90 95 100

Gly Asn Trp Arg Pro Pro Gly Ala Thr Pro Lys Gly Thr Ile Thr Val  
105 110 115

Asp Gly Gly Thr Tyr Asp Ile Tyr Glu Thr Leu Arg Val Asn Gln Pro  
120 125 130

Ser Ile Lys Gly Ile Ala Thr Phe Lys Gln Tyr Trp Ser Val Arg Arg  
135 140 145

Ser Lys Arg Thr Ser Gly Thr Ile Ser Val Ser Asn His Phe Arg Ala  
150 155 160 165

Trp Glu Asn Leu Gly Met Asn Met Gly Lys Met Tyr Glu Val Ala Leu  
170 175 180

Thr Val Glu Gly Tyr Gln Ser Ser Gly Ser Ala Asn Val Tyr Ser Asn  
185 190 195

Thr Leu Arg Ile Asn Gly Asn Pro Leu Ser Thr Ile Ser Asn Asp Glu  
200 205 210

Ser Ile Thr Leu Asp Lys Asn Asn  
215 220

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ATGAGACAAA AGAAATTGAC GTTGATTTTA GCCTTTT TAG TTTGTTTGC ACTAACCTTA 60

CCTGCAGAAA TAATTCAGGC A 81

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ATG AGA CAA AAG AAA TTG ACG TTG ATT TTA GCC TTT TTA GTT TGT TTT 48  
Met Arg Gln Lys Lys Leu Thr Leu Ile Leu Ala Phe Leu Val Cys Phe  
1 5 10 15

GCA CTA ACC TTA CCT GCA GAA ATA ATT CAG GCA 81  
Ala Leu Thr Leu Pro Ala Glu Ile Ile Gln Ala  
20 25

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal fragment

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Bacillus  
(B) SOURCE: 720/1

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Arg Gln Lys Lys Leu Thr Leu Ile Leu Ala Phe Leu Val Cys Phe  
1 5 10 15  
Ala Leu Thr Leu Pro Ala Glu Ile Ile Gln Ala  
20 25

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1513 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

15

(ii) MOLECULE TYPE: genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

AAATTGAATT GTGTATATCT AATGATAACG ACAAATCGTC ACTGTTTTTA AACTAATCTC 60

AAACCAATAC TTCTTTATTT AACGCTAACC ACTTGCAATC TTATCACAAG AACATTCTTT 120

ATAGGAACTT TCCCATTGTC AAGACGATAA AAAATCTTTT TCCCCTATTT TATCTTATCG 180

CCTTGATCGG TTTAATTTGT AAACCTTTATT TTAGTTTACG TGATGTTCCC TCATTCATAC 240

CATTAATCAC AGTTAACGCT AGAGTCATCT TTTTTCGGTT CTCAAAAATA CCTGAAGAAC 300

ATTTATGTCA TATTTTCTCA CGCCGCTCCA TAATGGAATA TATATACTCT TTTATACATA 360

TTAAGTAAAT TAGTATATAC TTGCGTTATC AAAATGTGAG ATAATCTAAT TGATCAAACA 420

AGCAGCTATC CAAAAACAC TGATGTTGAC CTCTTAAAGA AGTGTCAC TA TCTATGAAAA 480

GATAATTATC CAGTTTCAAA ATTTGAAATA GTGTGTATGG AATAGTTTGA ATGTCAACTG 540

CTGTGAAAGG AGGGTAGGTA GTACCGTAGA CTTCAATTACC AAAAATTAGT TGTAACAAAA 600

TTAAAAGGAG GAATGCCTAA TGAGACAAAA GAAATTGACG TTGATTTTAG CCTTTTTAGT 660

TTGTTTTGCA CTAACCTTAC CTGCAGAAAT AATTCAGGCA CAAATCGTCA CCGACAATTC 720

CATTGGCAAC CACGATGGCT ATGATTATGA ATTTTGGAAA GATAGCGGTG GCTCTGGGAC 780

AATGATTCTC AATCATGGCG GTACGTTTACG TGCCCAATGG AACAATGTGA ACAACATATT 840

ATTCCGTAAA GGTAACAAAT TCAATGAAAC ACAAACACAC CAACAAGTTG GTAACATGTC 900

CATAAACTAC GGAGCCAAC TCCAACCAAA TGGTAATGCG TATTTATGCG TCTATGGTTG 960

GACTGTTGAC CCTCTTGTCG AATATTATAT TGTCGACAGT TGGGGCAACT GGCGTCCACC 1020

AGGAGCAACG CCTAAGGGGA CCATCACTGT TGATGGAGGA ACATATGATA TCTACGAGAC 1080

TCTTAGAGTC AATCAACCCT CCATTAAGGG GATTGCCACA TTAAACAAT ATTGGAGTGT 1140

TCGAAGATCG AAACGCACGA GTGGCACGAT TTCTGTCAGC AACCACTTTA GAGCGTGGGA 1200  
AAACTTAGGG ATGAATATGG GGAAAATGTA TGAAGTCGCG CTTACTGTAG AAGGCTATCA 1260  
AAGTAGCGGA AGTGCTAATG TATATAGCAA TACACTAAGA ATTAACGGTA ACCCTCTCTC 1320  
AACTATTAGT AATGACGAGA GCATAACTTT GGATAAAAAC AATTAAAAAT CCTTATCTCT 1380  
TTCGGTTCAG TTCTCATTAT TTTCAAATAA CCTCCCGGTT GGATCTTTTC CAACGGGAGG 1440  
TTTTATTGGA AAGGTTAAGT ATAGTATACT CCGATTCCAT CCAGAGGAAT GCTTGAAACA 1500  
CCTCCGTCAC TAG 1513

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1513 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

AAATTGAATT GTGTATATCT AATGATAACG ACAAATCGTC ACTGTTTTTA AACTAATCTC 60

AAACCAATAC TTCTTTATTT AACGCTAACC ACTTGCAATC TTATCACAAG AACATTCTTT	120
ATAGGAACTT TCCCATTGTC AAGACGATAA AAAATCTTTT TCCCCTATTT TATCTTATCG	180
CCTTGATCGG TTTAATTTGT AAACCTTTATT TTAGTTTACG TGATGTTCCC TCATTCATAC	240
CATTAATCAC AGTTAACGCT AGAGTCATCT TTTTTCGGTT CTCAAAAATA CCTGAAGAAC	300
ATTTATGTCA TATTTTCTCA CGCCGCTCCA TAATGGAATA TATATACTCT TTTATACATA	360
TTAAGTAAAT TAGTATATAC TTGCGTTATC AAAATGTGAG ATAATCTAAT TGATCAAACA	420
AGCAGCTATC CAAAAACAC TGATGTTGAC CTCTTAAAGA AGTGTCAC TA TCTATGAAAA	480
GATAATTATC CAGTTTCAAA ATTTGAAATA GTGTGTATGG AATAGTTTGA ATGTCAACTG	540
CTGTGAAAGG AGGGTAGGTA GTACCGTAGA CTTTCATTACC AAAAATTAGT TGTAACAAAAA	600
TTAAAAGGAG GAATGCCTA ATG AGA CAA AAG AAA TTG ACG TTG ATT TTA GCC	652
Met Arg Gln Lys Lys Leu Thr Leu Ile Leu Ala	
-25 -20	
TTT TTA GTT TGT TTT GCA CTA ACC TTA CCT GCA GAA ATA ATT CAG GCA	700
Phe Leu Val Cys Phe Ala Leu Thr Leu Pro Ala Glu Ile Ile Gln Ala	
-15 -10 -5 -1	
CAA ATC GTC ACC GAC AAT TCC ATT GGC AAC CAC GAT GGC TAT GAT TAT	748
Gln Ile Val Thr Asp Asn Ser Ile Gly Asn His Asp Gly Tyr Asp Tyr	
1 5 10 15	
GAA TTT TGG AAA GAT AGC GGT GGC TCT GGG ACA ATG ATT CTC AAT CAT	796
Glu Phe Trp Lys Asp Ser Gly Gly Ser Gly Thr Met Ile Leu Asn His	
20 25 30	

GGC GGT ACG TTC AGT GCC CAA TGG AAC AAT GTT AAC AAC ATA TTA TTC	844
Gly Gly Thr Phe Ser Ala Gln Trp Asn Asn Val Asn Asn Ile Leu Phe	
35 40 45	
CGT AAA GGT AAA AAA TTC AAT GAA ACA CAA ACA CAC CAA CAA GTT GGT	892
Arg Lys Gly Lys Lys Phe Asn Glu Thr Gln Thr His Gln Gln Val Gly	
50 55 60	
AAC ATG TCC ATA AAC TAC GGA GCC AAC TTC CAA CCA AAT GGT AAT GCG	940
Asn Met Ser Ile Asn Tyr Gly Ala Asn Phe Gln Pro Asn Gly Asn Ala	
65 70 75 80	
TAT TTA TGC GTC TAT GGT TGG ACT GTT GAC CCT CTT GTC GAA TAT TAT	988
Tyr Leu Cys Val Tyr Gly Trp Thr Val Asp Pro Leu Val Glu Tyr Tyr	
85 90 95	
ATT GTC GAC AGT TGG GGC AAC TGG CGT CCA CCA GGA GCA ACG CCT AAG	1036
Ile Val Asp Ser Trp Gly Asn Trp Arg Pro Pro Gly Ala Thr Pro Lys	
100 105 110	
GGG ACC ATC ACT GTT GAT GGA GGA ACA TAT GAT ATC TAC GAG ACT CTT	1084
Gly Thr Ile Thr Val Asp Gly Gly Thr Tyr Asp Ile Tyr Glu Thr Leu	
115 120 125	
AGA GTC AAT CAA CCC TCC ATT AAG GGG ATT GCC ACA TTT AAA CAA TAT	1132
Arg Val Asn Gln Pro Ser Ile Lys Gly Ile Ala Thr Phe Lys Gln Tyr	
130 135 140	
TGG AGT GTT CGA AGA TCG AAA CGC ACG AGT GGC ACG ATT TCT GTC AGC	1180
Trp Ser Val Arg Arg Ser Lys Arg Thr Ser Gly Thr Ile Ser Val Ser	
145 150 155 160	
AAC CAC TTT AGA GCG TGG GAA AAC TTA GGG ATG AAT ATG GGG AAA ATG	1228
Asn His Phe Arg Ala Trp Glu Asn Leu Gly Met Asn Met Gly Lys Met	
165 170 175	



TAT GAA GTC GCG CTT ACT GTA GAA GGC TAT CAA AGT AGC GGA AGT GCT 1276  
Tyr Glu Val Ala Leu Thr Val Glu Gly Tyr Gln Ser Ser Gly Ser Ala  
180 185 190

AAT GTA TAT AGC AAT ACA CTA AGA ATT AAC GGT AAC CCT CTC TCA ACT 1324  
Asn Val Tyr Ser Asn Thr Leu Arg Ile Asn Gly Asn Pro Leu Ser Thr  
195 200 205

ATT AGT AAT GAC GAG AGC ATA ACT TTG GAT AAA AAC AAT TAAAAATCCT 1373  
Ile Ser Asn Asp Glu Ser Ile Thr Leu Asp Lys Asn Asn  
210 215 220

TATCTCTTTC GGTTCAAGTC TCATTATTTT CAAATAACCT CCCGGTTGGA TCTTTTCCAA 1433

CGGGAGGTTT TATTGGAAAG GTTAAGTATA GTATACTCCG ATTCCATCCA GAGGAATGCT 1493

TGAAACACCT CCGTCACTAG 1513

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 619 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

AAATTGAATT GTGTATATCT AATGATAACG ACAAATCGTC ACTGTTTTTA AACTAATCTC 60  
AAACCAATAC TTCTTTATTT AACGCTAACC ACTTGCAATC TTATCACAAG AACATTCTTT 120  
ATAGGAACTT TCCCATTTGC AAGACGATAA AAAATCTTTT TCCCCTATTT TATCTTATCG 180

CCTTGATCGG TTTAATTTGT AAACTTTATT TTAGTTTACG TGATGTTCCC TCATTCATAC 240  
CATTAAATCAC AGTTAACGCT AGAGTCATCT TTTTTCGGTT CTCAAAAATA CCTGAAGAAC 300  
ATTTATGTCA TATTTTCTCA CGCCGCTCCA TAATGGAATA TATATACTCT TTTATACATA 360  
TTAAGTAAAT TAGTATATAC TTGCGTTATC AAAATGTGAG ATAATCTAAT TGATCAAACA 420  
AGCAGCTATC CAAAAACAC TGATGTTGAC CTCTTAAAGA AGTGTCACCTA TCTATGAAAA 480  
GATAATTATC CAGTTTCAA AATTGAAATA GTGTGTATGG AATAGTTTGA ATGTCAACTG 540  
CTGTGAAAGG AGGGTAGGTA GTACCGTAGA CTTCATTACC AAAAATTAGT TGTAACAAAAA 600  
TTAAAAGGAG GAATGCCTA 619

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 150 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

TAAAAATCCT TATCTCTTTC GGTTGAGTTC TCATTATTTT CAAATAACCT CCCGGTTGGA 60  
TCTTTTCCAA CGGGAGGTTT TATTGGAAAG GTTAAGTATA GTATACTCCG ATTCCATCCA 120  
GAGGAATGCT TGAAACACCT CCGTCACTAG 150

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 56 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: nucleic acid (synthetic oligo-nucleotide)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CCCCCCTACG TAGCGGCCGC CCCGGCCGGT AACCTAGGAA GTCAGCGCCC TGCACC

56

(2) INFORMATION FOR SEQ ID NO:15:

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: nucleic acid (synthetic oligo-nucleotide)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CCCCCCTACG TAGGCCGGGG CGGCCGCGGT TACCTAGGGC CTCGTGATAC GCCTAT

56

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 31 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: lin ar

(ii) MOLECULE TYPE: nucleic acid (synthetic oligo-nucl otide)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

ACGAGGAAAG ATGCTGTTCT TGTAAATGAG T

31

(2) INFORMATION FOR SEQ ID NO:17:

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: nucleic acid (synthetic oligo-nucleotide)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

TACCTTGTCT ACAAACCCC

19

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: nucleic acid (synthetic oligo-nucleotide)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CGGTCGCCGC ATACACTA

18

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 36 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: nucleic acid (synthetic oligo-nucleotide)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CCCCCCCCCG GTAACCTGCA TTAATGAATC GGCCAA

36

10 (2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 39 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: nucleic acid (synthetic oligo-nucleotide)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CCCCCCCCCG GTTACCGTAT TTATTAACCTT CTCCTAGTA

39

(2) INFORMATION FOR SEQ ID NO:21:

20 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: singl  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: nucleic acid (synthetic oligonucleotide)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CCCCCCTCTA GATTAATTAA CCAAGCTTGG GATCCGTCGA CCTGCAGATC

50

(2) INFORMATION FOR SEQ ID NO:22:

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: nucleic acid (synthetic oligonucleotide)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CCCCCCTGAA ATCAGCTGGA CTAAAAGGGA TGCAATTTC

39

(2) INFORMATION FOR SEQ ID NO:23:

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: nucleic acid (synthetic oligonucleotide)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CCCCCCGTCG ACCGCATGCG CCGGCACAGC

30

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 39 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: nucleic acid (synthetic oligo-nucleotide)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CCCCCGCAT GCGCAAATCG TCACCGACAA TTCCATTGG

39

10 (2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 19 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: nucleic acid (synthetic oligo-nucleotide)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

TACCTTGTCT ACAAACCCC

19

(2) INFORMATION FOR SEQ ID NO:26:

- 20 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 185 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

TCATGTA	ACT	CGCCTTG	ATC	TATTTCA	TTT	GTATCAA	AGG	ATTTATA	CAC	AAACAAG	GAGA	60
CATCCAT	GCC	GGGTAA	AAGC	AGTATCG	TTC	CATCTAA	CAG	AGAAGGN	CTG	CATGAA	AAGGA	120
GGTGATG	GGT	TTTTCAT	CTT	AGGGATG	GACA	GAACAAT	ACG	GATGAAAA		GGAGAGG	GAT	180
GGAAA												

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- 5
- (A) LENGTH: 81 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

ATGAATTTGA	AAAGATTGAG	GCTGTTGTTT	GTGATGTGTA	TTGGATTGT	GCTGACACTG	60
ACGGCTGTGC	CGGCTCATGC	G				81

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- 15
- (A) LENGTH: 81 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

ATG	AAT	TTG	AAA	AGA	TTG	AGG	CTG	TTG	TTT	GTG	ATG	TGT	ATT	GGA	TTT	48
Met	Asn	Leu	Lys	Arg	Leu	Arg	Leu	Leu	Phe	Val	Met	Cys	Ile	Gly	Phe	
1					5				10					15		



GTG CTG ACA CTG ACG GCT GTG CCG GCT CAT GCG  
Val Leu Thr Leu Thr Ala Val Pro Ala His Ala  
20 25

81

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 amino acids

(B) TYPE: amino acid

5 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Met Asn Leu Lys Arg Leu Arg Leu Leu Phe Val Met Cys Ile Gly Phe  
1 5 10 15  
Val Leu Thr Leu Thr Ala Val Pro Ala His Ala  
20 25